

1642

TECH CENTER 1600/2900

1 2002

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#18

RAW SEQUENCE LISTING

DATE: 01/23/2002

PATENT APPLICATION: US/09/601,534B

TIME: 16:56:33

Input Set : A:\09601534.txt

Output Set: N:\CRF3\01232002\I601534B.raw

ENTERED

3 <110> APPLICANT: Dennler, Sylviane Gabrielle Nadine
 4 Gauthier, Jean Michel
 5 Huet, Staphane
 7 <120> TITLE OF INVENTION: Method of screening therapeutic agents
 9 <130> FILE REFERENCE: 1430-245 PF3402/USw
 11 <140> CURRENT APPLICATION NUMBER: US 09/601,534B
 12 <141> CURRENT FILING DATE: 2000-08-28
 14 <150> PRIOR APPLICATION NUMBER: PCT/EP99/00664
 15 <151> PRIOR FILING DATE: 1999-02-04
 17 <150> PRIOR APPLICATION NUMBER: GB 9802475.5
 18 <151> PRIOR FILING DATE: 1998-02-06
 20 <160> NUMBER OF SEQ ID NOS: 23
 22 <170> SOFTWARE: MS Word
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 81
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Artificial Sequence
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: Synthetic construct
 32 <400> SEQUENCE: 1
 33 agccagacaa gccagacaag ccagacaagc cagacaagcc agacaagcca gacaagccag 60
 34 acaagccaga caagccagac a 81
 37 <210> SEQ ID NO: 2
 38 <211> LENGTH: 81
 39 <212> TYPE: DNA
 40 <213> ORGANISM: Artificial Sequence
 42 <220> FEATURE:
 43 <223> OTHER INFORMATION: Synthetic construct
 45 <400> SEQUENCE: 2
 46 agacagacaa gacagacaag acagacaaga cagacaagac agacaagaca gacaagacag 60
 47 acaagacaga caagacagac a 81
 50 <210> SEQ ID NO: 3
 51 <211> LENGTH: 81
 52 <212> TYPE: DNA
 53 <213> ORGANISM: Artificial Sequence
 55 <220> FEATURE:
 56 <223> OTHER INFORMATION: Synthetic construct
 58 <400> SEQUENCE: 3
 59 agctacataa gctacataag ctacataagc tacataagct acataagcta cataagctac 60
 60 ataagctaca taagctacat a 81
 63 <210> SEQ ID NO: 4
 64 <211> LENGTH: 467
 65 <212> TYPE: PRT

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66 <213> ORGANISM: Homo sapiens
68 <400> SEQUENCE: 4
69 Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu
70 1 5 10 15
72 Gly Trp Lys Lys Ser Ala Gly Gly Ser Gly Gly Ala Gly Gly Gly Glu
73 20 25 30
75 Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu
76 35 40 45
78 Val Lys Lys Leu Lys Lys Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala
79 50 55 60
81 Ile Thr Thr Gln Asn Cys Asn Thr Lys Cys Val Thr Ile Pro Ser Thr
82 65 70 75 80
84 Cys Ser Glu Ile Trp Gly Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp
85 85 90 95
87 Asp Thr Thr Gly Leu Tyr Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp
88 100 105 110
90 Gly Arg Leu Gln Val Ser His Arg Lys Gly Leu Pro His Val Ile Tyr
91 115 120 125
93 Cys Arg Leu Trp Arg Trp Pro Asp Leu His Ser His His Glu Leu Lys
94 130 135 140
96 Ala Ile Glu Asn Cys Glu Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val
97 145 150 155 160
99 Cys Val Asn Pro Tyr His Tyr Gln Arg Val Glu Thr Pro Val Leu Pro
100 165 170 175
102 Pro Val Leu Val Pro Arg His Thr Glu Ile Leu Thr Glu Leu Pro Pro
103 180 185 190
105 Leu Asp Asp Tyr Thr His Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala
106 195 200 205
108 Gly Ile Glu Pro Gln Ser Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly
109 210 215 220
111 Tyr Ile Ser Glu Asp Gly Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser
112 225 230 235 240
114 Met Asp Thr Gly Ser Pro Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro
115 245 250 255
117 Val Asn His Ser Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala
118 260 265 270
120 Phe Trp Cys Ser Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu
121 275 280 285
123 Thr Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp
124 290 295 300
126 Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn
127 305 310 315 320
129 Arg Asn Ala Thr Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val
130 325 330 335
132 Arg Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp
133 340 345 350
135 Ser Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp
136 355 360 365
138 His Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile

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139      370      375      380
141 Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln
142 385      390      395      400
144 Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met
145      405      410      415
147 Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr
148      420      425      430
150 Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp
151      435      440      445
153 Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser
154      450      455      460
156 Ser Met Ser
157 465
160 <210> SEQ ID NO: 5
161 <211> LENGTH: 425
162 <212> TYPE: PRT
163 <213> ORGANISM: Homo sapiens
165 <400> SEQUENCE: 5
166 Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Ile Val Lys Arg Leu Leu
167 1      5      10      15
169 Gly Trp Lys Lys Gly Glu Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu
170      20      25      30
172 Lys Ala Val Lys Ser Leu Val Lys Lys Leu Lys Lys Thr Gly Gln Leu
173      35      40      45
175 Asp Glu Leu Glu Lys Ala Ile Thr Thr Gln Asn Val Asn Thr Lys Cys
176      50      55      60
178 Ile Thr Ile Pro Arg Ser Leu Asp Gly Arg Leu Gln Val Ser His Arg
179 65      70      75      80
181 Lys Gly Leu Pro His Val Ile Tyr Cys Arg Leu Trp Arg Trp Pro Asp
182      85      90      95
184 Leu His Ser His His Glu Leu Arg Ala Met Glu Leu Cys Glu Phe Ala
185      100      105      110
187 Phe Asn Met Lys Lys Asp Glu Val Cys Val Asn Pro Tyr His Tyr Gln
188      115      120      125
190 Arg Val Glu Thr Pro Val Leu Pro Pro Val Leu Val Pro Arg His Thr
191      130      135      140
193 Glu Ile Pro Ala Glu Phe Pro Pro Leu Asp Asp Tyr Ser His Ser Ile
194 145      150      155      160
196 Pro Glu Asn Thr Asn Phe Pro Ala Gly Ile Glu Pro Gln Ser Asn Ile
197      165      170      175
199 Pro Glu Thr Pro Pro Pro Gly Tyr Leu Ser Glu Asp Gly Glu Thr Ser
200      180      185      190
202 Asp His Gln Met Asn His Ser Met Asp Ala Gly Ser Pro Asn Leu Ser
203      195      200      205
205 Pro Asn Pro Met Ser Pro Ala His Asn Asn Leu Asp Leu Gln Pro Val
206      210      215      220
208 Thr Tyr Cys Glu Pro Ala Phe Trp Cys Ser Ile Ser Tyr Tyr Glu Leu
209 225      230      235      240
211 Asn Gln Arg Val Gly Glu Thr Phe His Ala Ser Gln Pro Ser Met Thr

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212                               245                               250                               255
214 Val Asp Gly Phe Thr Asp Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly
215                               260                               265                               270
217 Leu Leu Ser Asn Val Asn Arg Asn Ala Ala Val Glu Leu Thr Arg Arg
218                               275                               280                               285
220 His Ile Gly Arg Gly Val Arg Leu Tyr Tyr Ile Gly Gly Glu Val Phe
221                               290                               295                               300
223 Ala Glu Cys Leu Ser Asp Ser Ala Ile Phe Val Gln Ser Pro Asn Cys
224 305                               310                               315                               320
226 Asn Gln Arg Tyr Gly Trp His Pro Ala Thr Val Cys Lys Ile Pro Pro
227                               325                               330                               335
229 Gly Cys Asn Leu Lys Ile Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu
230                               340                               345                               350
232 Ala Gln Ser Val Asn Gln Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg
233                               355                               360                               365
235 Met Cys Thr Ile Arg Met Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr
236                               370                               375                               380
238 Arg Arg Gln Thr Val Thr Ser Thr Pro Cys Trp Ile Glu Leu His Leu
239 385                               390                               395                               400
241 Asn Gly Pro Leu Gln Trp Leu Asp Lys Val Leu Thr Gln Met Gly Ser
242                               405                               410                               415
244 Pro Ser Ile Arg Cys Ser Ser Val Ser
245                               420                               425
248 <210> SEQ ID NO: 6
249 <211> LENGTH: 39
250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:
254 <223> OTHER INFORMATION: Oligonucleotide
256 <400> SEQUENCE: 6
257 tcgagagcca gacaaaaagc cagacattta gccagacac
260 <210> SEQ ID NO: 7
261 <211> LENGTH: 39
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Oligonucleotide
268 <400> SEQUENCE: 7
269 tcgagtgtct ggctaaatgt ctggcttttt gtctggctc
272 <210> SEQ ID NO: 8
273 <211> LENGTH: 39
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: Oligonucleotide
280 <400> SEQUENCE: 8
281 tcgagagaca gacaaaaaga cagacattta gacagacac
284 <210> SEQ ID NO: 9
285 <211> LENGTH: 39

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286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Oligonucleotide
292 <400> SEQUENCE: 9
293 tcgagtgtct gtctaaatgt ctgtcttttt gtctgtctc          39
296 <210> SEQ ID NO: 10
297 <211> LENGTH: 39
298 <212> TYPE: DNA
299 <213> ORGANISM: Artificial Sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: Oligonucleotide
304 <400> SEQUENCE: 10
305 tcgagagcta cataaaaagc tacatattta gctacatac          39
307 <210> SEQ ID NO: 11
308 <211> LENGTH: 39
309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial Sequence
312 <220> FEATURE:
313 <223> OTHER INFORMATION: Oligonucleotide
315 <400> SEQUENCE: 11
316 tcgagtatgt agctaaatat gtagcttttt atgtagctc          39
319 <210> SEQ ID NO: 12
320 <211> LENGTH: 39
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial Sequence
324 <220> FEATURE:
325 <223> OTHER INFORMATION: Oligonucleotide
327 <400> SEQUENCE: 12
328 tcgagagcca gacaaggagc cagacaagga gccagacac          39
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332 <211> LENGTH: 40
333 <212> TYPE: DNA
334 <213> ORGANISM: Artificial Sequence
336 <220> FEATURE:
337 <223> OTHER INFORMATION: Oligonucleotide
339 <400> SEQUENCE: 13
340 ctcgagtgtc tggctccttg tctggctcct tgtctggctc          40
343 <210> SEQ ID NO: 14
344 <211> LENGTH: 39
345 <212> TYPE: DNA
346 <213> ORGANISM: Artificial Sequence
348 <220> FEATURE:
349 <223> OTHER INFORMATION: Oligonucleotide
352 <400> SEQUENCE: 14
353 tcgagagcta cataaaaagc tacatattta gctacatac          39
356 <210> SEQ ID NO: 15
357 <211> LENGTH: 39
358 <212> TYPE: DNA

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VERIFICATION SUMMARY

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